



00-617-F.ST25.txt
SEQUENCE LISTING

<110> Oregon Health & Science University
Hefeneider, Steven
Bennett, Robert
Seiss, Donald
Merkins, Louise

<120> Mammalian Cell Surface DNA Receptor

<130> 00-617-F

<140> US 10/619992

<141> 2003-07-15

<150> 09/921,099

<151> 2001-08-01

<160> 21

<170> PatentIn version 3.3

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gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat	3097
Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His	
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Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile	
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865 870 875 880	
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Phe Glu Thr Gln Arg Arg Thr Lys Glu Asp Pro Ile Ile Pro Phe	
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Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser	
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Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser	
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Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu	
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cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct	3625
Gln Gln Ala Lys Ser Asn Ser Leu Leu Gln Arg Glu Ala Asn Ala	
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Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His	
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ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gga	3715
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Pro Asp Gly Gln Ser Glu Pro	Ile Glu Glu Ile Leu	Asp Ile Gln	
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Ser Val Ser Ala Gly Asn Leu	Ile Leu Lys Thr His	Val Met Ser	
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Val Asn Ser			
1190			
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Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
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Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
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Pro Val Asn Phe Ala Leu Leu Gln Leu Val Gly Ala Gln Val Pro Asp
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His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu
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Val Ala Lys Lys Cys Val Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu
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Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg
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Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu
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Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu
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Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu
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Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu
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Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val
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Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly
225 230 235 240

His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys
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Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser
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Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala
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290 295 300

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Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro
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His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser
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Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val
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Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly
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Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile
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Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu
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580 585 590

Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe
595 600 605

Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr
610 615 620

Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn
625 630 635 640

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645 650 655

His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr
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Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser
675 680 685

Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro
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740 745 750

Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys
755 760 765

Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln
770 775 780

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Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala
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 820 825 830

Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile
 835 840 845

Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala
 850 855 860

Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu
 865 870 875 880

Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe
 885 890 895

Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser
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Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln
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Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val
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 995 1000 1005

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Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly
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 Lys Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu
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 Ser Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser
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 Glu Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met
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 Val Asn Ser
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 <213> Homo sapiens

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 tattatgttt tgggttactg gttatccaag ggaaacacctt tttaaaccaa caaaacaaaa 180
 aaaccgcccc gcagtccaaa gtaatttgtg ttcctaaaaa tggaatatgg aaagttaatt 240

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tgc	tat	aat	gaa	ttt	gat	gag	aat	gtg	cac	aaa	ccc	atc	agt	tta	ggt		697
Cys	Tyr	Asn	Glu	Phe	Asp	Glu	Asn	Val	His	Lys	Pro	Ile	Ser	Leu	Gly		
20								25							30		
tgt	tca	cac	act	gtt	tgc	aag	acc	tgc	ttg	aat	aaa	ctt	cat	cga	aaa		745
Cys	Ser	His	Thr	Val	Cys	Lys	Thr	Cys	Leu	Asn	Lys	Leu	His	Arg	Lys		
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gct	tgt	cct	ttt	gac	cag	act	gcc	atc	aac	aca	gat	att	gat	gta	ctt		793
Ala	Cys	Pro	Phe	Asp	Gln	Thr	Ala	Ile	Asn	Thr	Asp	Ile	Asp	Val	Leu		
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cct	gtc	aac	ttc	gca	ctt	ctc	cag	tta	gtt	gga	gcc	cag	gta	cca	gat		841
Pro	Val	Asn	Phe	Ala	Leu	Leu	Gln	Leu	Val	Gly	Ala	Gln	Val	Pro	Asp		
65							70								80		
cat	cag	tca	att	aag	tta	agt	aat	cta	ggg	gag	aat	aaa	cac	tat	gag		889
His	Gln	Ser	Ile	Lys	Leu	Ser	Asn	Leu	Gly	Glu	Asn	Lys	His	Tyr	Glu		
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gtt	gca	aag	aaa	tgc	gtt	gag	gat	ttg	gca	ctc	tac	tta	aaa	cca	cta		937
Val	Ala	Lys	Lys	Cys	Val	Glu	Asp	Leu	Ala	Leu	Tyr	Leu	Lys	Pro	Leu		
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agt	gga	ggt	aaa	ggt	gta	gct	agc	ttg	aac	cag	agt	gca	ctg	agc	cgt		985
Ser	Gly	Gly	Lys	Gly	Val	Ala	Ser	Leu	Asn	Gln	Ser	Ala	Leu	Ser	Arg		
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cca	atg	caa	agg	aaa	ctg	gtg	aca	ctt	gta	aac	tgt	caa	ctg	gtg	gag		1033
Pro	Met	Gln	Arg	Lys	Leu	Val	Thr	Leu	Val	Asn	Cys	Gln	Leu	Val	Glu		
							130								140		
gaa	gaa	ggt	cgt	gta	aga	gcc	atg	cga	gca	gct	cgt	tcc	ctt	gga	gaa		1081
Glu	Glu	Gly	Arg	Val	Arg	Ala	Met	Arg	Ala	Ala	Arg	Ser	Leu	Gly	Glu		
							145								155		
aga	act	gta	aca	gaa	ctg	ata	tta	cag	cac	cag	aac	cct	cag	cag	ttg		1129
Arg	Thr	Val	Thr	Glu	Leu	Ile	Leu	Gln	His	Gln	Asn	Pro	Gln	Gln	Leu		
							165								170		
tct	gcc	aat	cta	tgg	gcc	gct	gtc	agg	gct	cga	gga	tgc	cag	ttt	tta		1177
Ser	Ala	Asn	Leu	Trp	Ala	Ala	Val	Arg	Ala	Arg	Gly	Cys	Gln	Phe	Leu		
							180								185		
ggg	cca	gct	atg	caa	gaa	gag	gcc	ttg	aag	ctg	gtg	tta	ctg	gca	tta		1225
Gly	Pro	Ala	Met	Gln	Glu	Glu	Ala	Leu	Lys	Leu	Val	Leu	Leu	Ala	Leu		

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cag aga cta gaa cca aga ttt cct cag gca tca aaa aca agt att ggt Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly 225 230 235 240			1321
cat gtt gtg caa cta ctg tat cga gct tct tgt ttt aag gtt acc aaa His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys 245 250 255			1369
aga gat gaa gac tct tcc cta atg cag ctg aag gag gaa ttt cggtt Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser 260 265 270			1417
tat gaa gca tta cgc aga gaa cat gat gcc caa att gtt cat att gcc Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala 275 280 285			1465
atg gaa gca gga ctc cgt att tca cct gaa cag tgg tcc tct ctt ttg Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu 290 295 300			1513
tat ggt gat ttg gct cat aaa tca cac atg cag tct atc att gat aag Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys 305 310 315 320			1561
cta cag tct cca gag tca ttt gca aag agt gtc cag gaa ttg aca att Leu Gln Ser Pro Glu Ser Phe Ala Lys Ser Val Gln Glu Leu Thr Ile 325 330 335			1609
gtt ttg caa cga aca ggt gac cca gct aac tta aat aga ctg agg cct Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro 340 345 350			1657
cat tta gag ctt ctt gca aac ata gac cct aat cca gac gct gtt tca His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser 355 360 365			1705
cca act tgg gag cag ctg gaa aat gca atg gta gct gtt aaa aca gta Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val 370 375 380			1753
gtt cat ggc ctt gtg gac ttc ata caa aat tat agt aga aaa ggc cat Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His 385 390 395 400			1801
gag acc cct cag cct cag cca aac agc aaa tac aag act agc atg tgc Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys 405 410 415			1849
cga gat ttg cga cag cag ggg ggt tgt cca cga gga aca aat tgt aca Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr 420 425 430			1897
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aag atc aat gcc act gta aga acg ttt cct ctt cta aat aaa gtt ggt			1993

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Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly			
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Val Asn Asn Thr Val Thr Thr Ala Gly Asn Val Ile Ser Val Ile			
465	470	475	480
gga agt act gaa aca aca ggg aaa att gtt cca agt aca aac gga att			2089
Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile			
485	490	495	
tca aat gca gaa aac agt gtt tcc cag cta atc tca cgt agt act gac			2137
Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp			
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agt acc tta aga gct ctg gag acc gtg aag aaa gtg gga aag gtt ggc			2185
Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly			
515	520	525	
gct aat ggt cag aat gct gct ggg ccc tct gca gat tct gta act gaa			2233
Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu			
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aat aaa att ggt tct cca ccc aag act cct gta agt aat gta gca gct			2281
Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala			
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acc tca gct ggg ccc tct aat gtt gga aca gag ctg aat tct gtg cct			2329
Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro			
565	570	575	
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Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His			
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Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe			
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Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr			
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Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn			
625	630	635	640
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Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp			
645	650	655	
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His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr			
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Gln Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser			
675	680	685	
gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct			2713
Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro			
690	695	700	

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atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met 705 710 715 720	2761
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aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu 740 745 750	2857
cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys 755 760 765	2905
acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln 770 775 780	2953
tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala 785 790 795 800	3001
aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt Thr Gln Ser Pro Thr Pro Ser Pro Leu Phe Ser Val Asp Phe Arg 805 810 815	3049
gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His 820 825 830	3097
ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile 835 840 845	3145
aat gcc att gat tca gag ccc aaa gat gtc att gct aat tca aat gct Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala 850 855 860	3193
gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu 865 870 875 880	3241
ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe 885 890 895	3289
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aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser 945 950 955 960	3481

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ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu 980 985 990	3577
cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala 995 1000 1005	3625
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ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gag Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Glu 1025 1030 1035	3715
tta cag agt gat tat aca gaa gat gca aca gat act aaa cct gat Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro Asp 1040 1045 1050	3760
agg gat atc gag tta gag ctt tca gca ctt gat act gat gaa cct Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu Pro 1055 1060 1065	3805
gat gga caa agt gaa cca att gaa gag atc ttg gac ata cag ctt Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln Leu 1070 1075 1080	3850
ggt atc agt tct caa aat gat cag ttg cta aat gga atg gca gtg Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala Val 1085 1090 1095	3895
gaa aat ggg cat cca gta cag cag cac caa aag gag cca cca aag Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro Lys 1100 1105 1110	3940
cag aag aaa cag agt tta ggt gaa gac cat gtg att ctg gag gag Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu Glu 1115 1120 1125	3985
caa aaa aca att ctg ccg gta act tct tgc ttt agc cag cca ctc Gln Lys Thr Ile Leu Pro Val Thr Ser Cys Phe Ser Gln Pro Leu 1130 1135 1140	4030
cca gtg tct att agc aat gca agt tgc ctc ccc atc acc aca tct Pro Val Ser Ile Ser Asn Ala Ser Cys Leu Pro Ile Thr Thr Ser 1145 1150 1155	4075
gtc agt gct ggc aac ctc att ctg aaa act cat gtt atg tct gaa Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser Glu 1160 1165 1170	4120
gat aaa aac gac ttt tta aaa cct gtt gca aat ggg aag atg gtt Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met Val 1175 1180 1185	4165
aac agc tga aaggagggttc atctttcaaa tttgtgacca caccatggaa	4214
Asn Ser	

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1190

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aaaaagatat tactggggc atccatttcc tgtggactct ttgatacttc aagcccttt 4334
gcatttagcat tatg 4348

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<212> PRT
<213> *Homo sapiens*

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Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
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Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
35 40 45

Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
50 55 60

Pro Val Asn Phe Ala Leu Leu Gln Leu Val Gly Ala Gln Val Pro Asp
65 70 75 80

His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu
85 90 95

Val Ala Lys Lys Val Cys Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu
100 105 110

Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg
115 120 125

Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu
130 135 140

Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu
145 150 155 160

Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu
165 170 175

Ser Ala Asn Leu Trp Ala Ala Val Arg Ala Arg Gly Cys Gln Phe Leu
180 185 190

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Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu
195 200 205

Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val
210 215 220

Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly
225 230 235 240

His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys
245 250 255

Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser
260 265 270

Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala
275 280 285

Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu
290 295 300

Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys
305 310 315 320

Leu Gln Ser Pro Glu Ser Phe Ala Lys Ser Val Gln Glu Leu Thr Ile
325 330 335

Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro
340 345 350

His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser
355 360 365

Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val
370 375 380

Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His
385 390 395 400

Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys
405 410 415

Arg Asp Leu Arg Gln Gln Gly Cys Pro Arg Gly Thr Asn Cys Thr
420 425 430

Phe Ala His Ser Gln Glu Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys
435 440 445

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Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly
450 455 460

Val Asn Asn Thr Val Thr Thr Ala Gly Asn Val Ile Ser Val Ile
465 470 475 480

Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile
485 490 495

Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp
500 505 510

Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly
515 520 525

Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu
530 535 540

Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala
545 550 555 560

Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro
565 570 575

Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His
580 585 590

Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe
595 600 605

Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr
610 615 620

Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn
625 630 635 640

Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp
645 650 655

His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr
660 665 670

Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser
675 680 685

Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro
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690

695

700

Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met
 705 710 715 720

Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr
 725 730 735

Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu
 740 745 750

Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys
 755 760 765

Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln
 770 775 780

Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala
 785 790 795 800

Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg
 805 810 815

Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His
 820 825 830

Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile
 835 840 845

Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala
 850 855 860

Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu
 865 870 875 880

Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe
 885 890 895

Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser
 900 905 910

Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln
 915 920 925

Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val
 930 935 940

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Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser
 945 950 955 960

Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser
 965 970 975

Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu
 980 985 990

Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala
 995 1000 1005

Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His
 1010 1015 1020

Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Glu
 1025 1030 1035

Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro Asp
 1040 1045 1050

Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu Pro
 1055 1060 1065

Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln Leu
 1070 1075 1080

Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala Val
 1085 1090 1095

Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro Lys
 1100 1105 1110

Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu Glu
 1115 1120 1125

Gln Lys Thr Ile Leu Pro Val Thr Ser Cys Phe Ser Gln Pro Leu
 1130 1135 1140

Pro Val Ser Ile Ser Asn Ala Ser Cys Leu Pro Ile Thr Thr Ser
 1145 1150 1155

Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser Glu
 1160 1165 1170

Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met Val
 1175 1180 1185

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Asn Ser
1190

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<211> 39
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> PCR primer 1 for cloning DNA-R

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<210> 6
<211> 26
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> PCR primer 2 for cloning DNA-R

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<211> 574
<212> PRT
<213> Homo sapiens

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Val Cys Glu Asp Val Phe Ser Leu Gln Gly Asp Lys Val Pro Arg Leu
35 40 45

Leu Leu Cys Gly His Thr Val Cys His Asp Cys Leu Thr Arg Leu Pro
50 55 60

Leu His Gly Arg Ala Ile Arg Cys Pro Phe Asp Arg Gln Val Thr Asp
65 70 75 80

Leu Gly Asp Ser Gly Val Trp Gly Leu Lys Lys Asn Phe Ala Leu Leu
85 90 95

Glu Leu Leu Glu Arg Leu Gln Asn Gly Pro Ile Gly Gln Tyr Gly Ala
100 105 110

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Ala Glu Glu Ser Ile Gly Ile Ser Gly Glu Ser Ile Ile Arg Cys Asp
115 120 125

Glu Asp Glu Ala His Leu Ala Ser Val Tyr Cys Thr Val Cys Ala Thr
130 135 140

His Leu Cys Ser Glu Cys Ser Gln Val Thr His Ser Thr Lys Thr Leu
145 150 155 160

Ala Lys His Arg Arg Val Pro Leu Ala Asp Lys Pro His Glu Lys Thr
165 170 175

Met Cys Ser Gln His Gln Val His Ala Ile Glu Phe Val Cys Leu Glu
180 185 190

Glu Gly Cys Gln Thr Ser Pro Leu Met Cys Cys Val Cys Lys Glu Tyr
195 200 205

Gly Lys His Gln Gly His Lys His Ser Val Leu Glu Pro Glu Ala Asn
210 215 220

Gln Ile Arg Ala Ser Ile Leu Asp Met Ala His Cys Ile Arg Thr Phe
225 230 235 240

Thr Glu Glu Ile Ser Asp Tyr Ser Arg Lys Leu Val Gly Ile Val Gln
245 250 255

His Ile Glu Gly Gly Glu Gln Ile Val Glu Asp Gly Ile Gly Met Ala
260 265 270

His Thr Glu His Val Pro Gly Thr Ala Glu Asn Ala Arg Ser Cys Ile
275 280 285

Arg Ala Tyr Phe Tyr Asp Leu His Glu Thr Leu Cys Arg Gln Glu Glu
290 295 300

Met Ala Leu Ser Val Val Asp Ala His Val Arg Glu Lys Leu Ile Trp
305 310 315 320

Leu Arg Gln Gln Gln Glu Asp Met Thr Ile Leu Leu Ser Glu Val Ser
325 330 335

Ala Ala Cys Leu His Cys Glu Lys Thr Leu Gln Gln Asp Asp Cys Arg
340 345 350

Val Val Leu Ala Lys Gln Glu Ile Thr Arg Leu Leu Thr Glu Leu Gln
355 360 365

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Lys Gln Gln Gln Gln Phe Thr Glu Val Ala Asp His Ile Gln Leu Asp
370 375 380

Ala Ser Ile Pro Val Thr Phe Thr Lys Asp Asn Arg Val His Ile Gly
385 390 395 400

Pro Lys Met Glu Ile Arg Val Val Thr Leu Gly Leu Asp Gly Ala Gly
405 410 415

Lys Thr Thr Ile Leu Phe Lys Leu Lys Gln Asp Glu Phe Met Gln Pro
420 425 430

Ile Pro Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Leu
435 440 445

Lys Phe Thr Ile Trp Asp Val Gly Gly Lys His Lys Leu Arg Pro Leu
450 455 460

Trp Lys His Tyr Tyr Leu Asn Thr Gln Ala Val Val Phe Val Val Asp
465 470 475 480

Ser Ser His Arg Asp Arg Ile Ser Glu Ala His Ser Glu Leu Ala Lys
485 490 495

Leu Leu Thr Glu Lys Glu Leu Arg Asp Ala Leu Leu Leu Ile Phe Ala
500 505 510

Asn Lys Gln Asp Val Ala Gly Ala Leu Ser Val Glu Glu Ile Thr Glu
515 520 525

Leu Leu Ser Leu His Lys Leu Cys Cys Gly Arg Ser Trp Tyr Ile Gln
530 535 540

Gly Cys Asp Ala Arg Ser Gly Met Gly Leu Tyr Glu Gly Leu Asp Trp
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<212> PRT
<213> Homo sapiens

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Ile Cys Pro Ile Cys Ser Gly Val Leu Glu Glu Pro Val Gln Ala Pro
20 25 30

His Cys Glu His Ala Phe Cys Asn Ala Cys Ile Thr Gln Trp Phe Ser
35 40 45

Gln Gln Gln Thr Cys Pro Val Asp Arg Ser Val Val Thr Val Ala His
50 55 60

Leu Arg Pro Val Pro Arg Ile Met Arg Asn Met Leu Ser Lys Leu Gln
65 70 75 80

Ile Ala Cys Asp Asn Ala Val Phe Gly Cys Ser Ala Val Val Arg Leu
85 90 95

Asp Asn Leu Met Ser His Leu Ser Asp Cys Glu His Asn Pro Lys Arg
100 105 110

Pro Val Thr Cys Glu Gln Gly Cys Gly Leu Glu Met Pro Lys Asp Glu
115 120 125

Leu Pro Asn His Asn Cys Ile Lys His Leu Arg Ser Val Val Gln Gln
130 135 140

Gln Gln Thr Arg Ile Ala Glu Leu Glu Lys Thr Ser Ala Glu His Lys
145 150 155 160

His Gln Leu Ala Glu Gln Lys Arg Asp Ile Gln Leu Leu Lys Ala Tyr
165 170 175

Met Arg Ala Ile Arg Ser Val Asn Pro Asn Leu Gln Asn Leu Glu Glu
180 185 190

Thr Ile Glu Tyr Asn Glu Ile Leu Glu Trp Val Asn Ser Leu Gln Pro
195 200 205

Ala Arg Val Thr Arg Trp Gly Gly Met Ile Ser Thr Pro Asp Ala Val
210 215 220

Leu Gln Ala Val Ile Lys Arg Ser Leu Val Glu Ser Gly Cys Pro Ala
225 230 235 240

Ser Ile Val Asn Glu Leu Ile Glu Asn Ala His Glu Arg Ser Trp Pro
245 250 255

Gln Gly Leu Ala Thr Leu Glu Thr Arg Gln Met Asn Arg Arg Tyr Tyr
Page 25

260

265

270

Glu Asn Tyr Val Ala Lys Arg Ile Pro Gly Lys Gln Ala Val Val Val
 275 280 285

Met Ala Cys Glu Asn Gln His Met Gly Asp Asp Met Val Gln Glu Pro
 290 295 300

Gly Leu Val Met Ile Phe Ala His Gly Val Glu Glu Ile
 305 310 315

<210> 9
 <211> 202
 <212> PRT
 <213> Caenorhabditis elegans

<400> 9

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Ala Leu Lys Asn Ser Gln Arg Leu Ser Val Arg Gly Ser Ile Gln Ser
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Asn Met Ser Ser Arg Thr Asp Gly Ile Leu Gln Arg Arg Leu Asp Glu
 35 40 45

Thr Glu Arg Lys Leu Ala Lys Thr Ser Ala Glu Leu Lys Ala Lys Asp
 50 55 60

Glu Lys Leu Lys Lys Glu Thr Ala Ser Leu Glu Ala Ser Arg Glu Ala
 65 70 75 80

His Arg Leu Leu Gln Glu Glu Ser Asn Lys Ser Lys Val Ser Val Met
 85 90 95

Arg Leu Thr Phe Lys Leu Asn Arg Ile Thr His Glu Ser Val Lys Glu
 100 105 110

Gln Ala Val Leu Lys Lys Leu Leu Asp Cys Glu Thr Arg Leu Ala
 115 120 125

Thr Tyr Ser Glu Cys Leu Val Cys Tyr Gln Lys Phe Asp Glu Asn Thr
 130 135 140

Arg Ile Pro Arg Val Met Asp Cys Gly His Thr Leu Cys Asp Phe Cys
 145 150 155 160

Ile Asn Gln Ile Val Lys Met Ala Gly Cys Tyr Ser Ala Thr Cys Pro
 Page 26

165

170

175

Phe Asp Arg Val Arg Ile Phe Gly Phe Gly Lys Ser Arg Arg Leu Glu
 180 185 190

Asp Arg Pro Cys Asn Arg Phe Ile Met Lys
 195 200

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<400> 10

Met Ala Pro Ile Arg Arg Ser Ser Arg Leu Ala Glu Arg Tyr Asp Ala
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Ile Glu Ser Lys Lys Arg Ser Leu Lys Arg Leu Glu Glu Gln Ile Lys
 20 25 30

Ala Glu Glu Glu Gln Phe Ser Asp Lys Met Lys Gln Leu Glu Asp Glu
 35 40 45

Ile Lys Ile Lys Glu Gln Val Ile Thr Met Phe Lys Arg Lys Thr Val
 50 55 60

Arg Arg Glu Trp Met Arg Asn Ser Arg Gln Ala Thr Thr Asn Ile Asn
 65 70 75 80

Ile Ala Gln Ile Glu Ser Leu Lys Leu Gln Leu Glu Glu Gly Glu Lys
 85 90 95

Asp Ile Ala Glu Ala Glu Lys Gln Ala Glu Pro Thr Thr Pro Gln Gln
 100 105 110

Glu Ala Glu Leu Ser Glu Thr Phe Lys Gln Met Val Arg Asp Arg Met
 115 120 125

Lys Val Lys Asp Val Asp Glu Lys Leu Leu Gln Gln Tyr Met Lys Lys
 130 135 140

Glu Asn Val Glu Phe Glu Trp Arg Ser Cys Phe Ile Cys Thr Met Glu
 145 150 155 160

Tyr Ser Arg Thr Asp Lys Asn Leu His Pro Ile Ile Leu Asn Cys Gly
 165 170 175

His Asn Leu Cys Arg Ser Cys Ile Asn Lys Leu Thr Gly Asn Gly Ile
 Page 27

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180

185

190

Val Lys Cys Pro Phe Asp Arg Leu Asp Thr Arg Val Arg Val Thr Gly
 195 200 205

Leu Pro Arg Asn Leu Ala Leu Ile Asn Leu
 210 215

<210> 11
 <211> 1048
 <212> PRT
 <213> *Caenorhabditis elegans*

<400> 11

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Ser Ile Cys Asn Arg His Phe Asn Glu Thr Phe Leu Pro Val Ser Leu
 20 25 30

Ile Cys Gly His Val Ile Cys Arg Lys Cys Ala Glu Lys Pro Glu Asn
 35 40 45

Gln Thr Lys Pro Cys Pro His Asp Asp Trp Lys Thr Thr His Ser Pro
 50 55 60

Ser Glu Tyr Pro Asn Asn Val Ala Leu Leu Ser Val Ile Phe Pro Arg
 65 70 75 80

Lys Gln Cys Met Thr Leu Ser Gly Ala Val Ser Glu Ala Glu Lys Arg
 85 90 95

Val Asp Gln Leu Ser Ile Gln Ile Ala Lys Phe Phe Arg Glu Ala Asp
 100 105 110

Ser Glu Arg Gly Gly Thr Val Ser Ser Arg Glu Ile Ser Arg Thr Leu
 115 120 125

Gln Arg Lys Val Leu Ala Leu Leu Cys Tyr Gln Trp Arg Glu Val Asp
 130 135 140

Gly Arg Leu Lys Thr Leu Lys Met Cys Arg Gly Ile Ser Glu Arg Val
 145 150 155 160

Met Ile Glu Ile Ile Leu Ser Ile Gln Ser Asn Thr His Val Ser Ser
 165 170 175

Gln Leu Trp Ser Ala Val Arg Ala Arg Gly Cys Gln Phe Leu Gly Pro
 Page 28

180

185

190

Ala Met Gln Asp Asp Val Leu Arg Leu Ile Leu Met Thr Leu Glu Thr
 195 200 205

Gly Glu Cys Ile Ala Arg Lys Asn Leu Val Met Tyr Val Val Gln Thr
 210 215 220

Leu Ala Ser Asp Tyr Pro Gln Val Ser Lys Thr Cys Val Gly His Val
 225 230 235 240

Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Asn Val Leu Lys Arg Asp
 245 250 255

Gly Glu Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Thr Tyr Glu
 260 265 270

Ser Leu Arg Arg Glu His Asp Ser Gln Ile Val Gln Ile Ala Phe Glu
 275 280 285

Ser Gly Leu Arg Ile Gly Pro Asp Gln Trp Ser Ala Leu Leu Tyr Ala
 290 295 300

Asp Gln Ser His Arg Ser His Met Gln Ser Ile Ile Asp Lys Leu Gln
 305 310 315 320

Ser Lys Asn Ser Tyr Gln Gln Gly Val Glu Glu Leu Arg Ala Leu Ala
 325 330 335

Gly Ser Gln Thr Ser Met Leu Val Pro Ala Tyr Arg Tyr Phe Leu Thr
 340 345 350

Gln Val Ile Pro Cys Leu Glu Phe Phe Ala Gly Ile Glu His Glu Asp
 355 360 365

Thr Ser Met Arg Met Ile Gly Asp Ala Leu His Gln Ile Arg Ile Leu
 370 375 380

Leu Lys Leu His Cys Ser Gln Asp Asp Leu Arg Lys Met Pro Lys Glu
 385 390 395 400

Glu Arg Arg Gly Val Ile Leu Gln Ala Glu Val Pro Gly Gly Met Gly
 405 410 415

Gly Gly Pro Gly Gly Ser Gly Gly Ala Glu Ala Gly Arg Ile Gly Gly
 420 425 430

00-617-F.ST25.txt

Leu His Pro Leu Tyr Ser Gln Ile Asp Glu Thr Gly Arg Ser Ile Ser
 435 440 445

Arg Thr Asn Pro Lys Asp Asn Ser His Asn Ser Pro Gln Thr Pro Pro
 450 455 460

Lys Gln Pro Arg Gln Lys Arg Tyr Gln Met Gly Ile Pro Pro Asn Arg
 465 470 475 480

Met Gly Tyr Ser Ser Asp Ala Pro Pro Phe Ile Pro Ser His Gln Gln
 485 490 495

Gln Pro Pro Pro Gln Phe Phe Asn Ser Gln His Leu Pro Gln Arg Phe
 500 505 510

Arg Gly Gly Arg Gln Arg Gly Ala Pro Pro Pro Pro Pro Gln Pro
 515 520 525

Met Pro Met Leu Ile Gly Tyr Asp Met Pro Gly Ala Pro Met Met Gln
 530 535 540

Ala Thr Glu Val Leu Thr Ala Asp Gly Gln Met Val Asn Gly Thr Pro
 545 550 555 560

Gln Arg Val Val Ile Met Gln Ser Pro Thr His Leu Pro Gly Gly Pro
 565 570 575

Val Val Met Ile Pro Gln Gln Met Val Pro Pro Pro Gln Ser Met
 580 585 590

Thr Pro Val Gly Gly Pro Met Gly Pro Met Gly Pro Met Thr Pro Ser
 595 600 605

Ile Pro Val Gln Val Pro Pro Asn Thr Met Trp Thr Ala Thr Ser Pro
 610 615 620

Thr Gly Ser Val Ile Tyr Pro Ala Ala Ser Pro Pro Gly Gln Pro Pro
 625 630 635 640

His Thr Ile Trp Ile Gln Ser Ile Gly Val Phe Lys Arg Lys Ser Asn
 645 650 655

Phe Leu Lys Ile Val Arg Lys Ile Ser Phe Phe Leu Asn Phe Tyr Asp
 660 665 670

Phe Phe Leu Ile Leu Arg Lys Leu Lys Lys Glu Lys Lys Gly Ala Asp
 675 680 685

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Ile Glu Phe Phe Glu Lys Ile Lys Ser Thr Asp Phe Lys Lys Tyr Pro
690 695 700

Ser Ser Phe Ser Arg Thr Asp Gly Asn Met Phe Pro Met Phe Asp Arg
705 710 715 720

Gly Ser Gly Gly Met Val Trp Gly Pro Gly Thr Met Leu Arg Glu Ser
725 730 735

Gly Ala Asp Ala Glu Gln Leu Leu Ala Lys Arg Tyr Glu Ile Leu Lys
740 745 750

Arg Leu Gln Pro Ser Glu Asp Asp Asp Pro Glu Asp Gly Gly Ile
755 760 765

Gly His Val Ser Tyr Thr Val Ala Ser Ser Val Leu Asp Asp Arg Met
770 775 780

Asp His His Pro Leu Thr Met Ile Pro Val Pro Thr Ile Asp Leu Pro
785 790 795 800

Ala Ile Pro Ile Ser Phe Ala Asn Met Pro Thr Glu Glu Thr Met Thr
805 810 815

Met Ile Gly Glu Met Val Gln Asn Arg Pro Arg Ala Pro Ser Leu Thr
820 825 830

Ala Pro Ser Ser Asn Gln Pro Met Asn Val Asn Ala Ser Ala Ser Ala
835 840 845

Thr Val Gln Ala Glu Cys Glu Asn Arg Lys Ile Leu Asp Phe Pro Leu
850 855 860

Lys Tyr Arg Lys Met Thr Leu Met Phe Glu Lys Val Ser Thr Cys Phe
865 870 875 880

His Val Thr Leu Leu Lys Asp Tyr Met Val Phe Tyr Val Leu Asn Thr
885 890 895

Leu Asn Phe Ala Ser Arg Trp Pro Arg Arg Arg Arg Ala Ala Thr Ile
900 905 910

Pro Gln Pro Val Ile Pro Met Val Gln Val Pro Val Gln Val Pro Ile
915 920 925

Val Pro Ala Glu Asn Phe Asn Pro Asn Val Pro Pro Pro Pro Pro Pro
930 935 940

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Pro	Gln	Gly	Gln	Pro	Met	Leu	Val	Asp	Ser	Ala	Ile	Gly	Leu	Leu	Thr
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Pro	Ile	Arg	Pro	Ile	Leu	Val	Ala	His	Pro	Gln	Asn	Val	Val	Ser	Asn
	965					970						975			
Ser	Leu	Asp	Lys	Ile	Val	Asp	Val	Lys	Glu	Arg	Ile	Ser	Glu	Ala	Gln
	980				985							990			
Gly	Asn	Ala	Ser	Glu	Ala	Glu	Asn	Ala	His	Leu	Arg	Met	Glu	Leu	Arg
	995				1000						1005				
Met	Ala	Glu	Ser	Gln	Met	Ala	His	Leu	Asp	Pro	Tyr	Thr	Lys	Asn	
1010		1015							1020						
Asn	Cys	Leu	Leu	Arg	Ala	Leu	Gln	Gln	Val	Asp	Met	Glu	Leu	Gln	
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Gln	Leu	His	Leu	Asn	Pro	Thr	Val	Glu	Gly						
1040			1045												
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															112
Met	Pro	Gly	Phe	Asp	Tyr	Lys	Phe	Leu							
1					5										
gag	aag	ccc	aag	cga	cgg	ctg	ctg	tgc	cca	ctg	tgc	ggg	aag	ccc	atg
Glu	Lys	Pro	Lys	Arg	Arg	Leu	Leu	Cys	Pro	Leu	Cys	Gly	Lys	Pro	Met
10		15					20						25		
cgc	gag	cct	gtg	cag	gtt	tcc	acc	tgc	ggc	cac	cgt	ttc	tgc	gat	acc
Arg	Glu	Pro	Val	Gln	Val	Ser	Thr	Cys	Gly	His	Arg	Phe	Cys	Asp	Thr
30				35						40					208
tgc	ctg	cag	gag	ttc	ctc	agt	gaa	gga	gtc	ttc	aag	tgc	cct	gag	gac
Cys	Leu	Gln	Glu	Phe	Leu	Ser	Glu	Gly	Val	Phe	Lys	Cys	Pro	Glu	Asp
45				50							55				256
cag	ctt	cct	ctg	gac	tat	gcc	aag	atc	tac	cca	gac	ccg	gag	ctg	gaa
Gln	Leu	Pro	Leu	Asp	Tyr	Ala	Lys	Ile	Tyr	Pro	Asp	Pro	Glu	Leu	Glu
60				65						70					304

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gta caa gta ttg ggc ctg cct atc cgc tgc atc cac agt gag gag ggc Val Gln Val Leu Gly Leu Pro Ile Arg Cys Ile His Ser Glu Glu Gly 75 80 85	352
tgc cgc tgg agt ggg cca cta cgt cat cta cag ggc cac ctg aat acc Cys Arg Trp Ser Gly Pro Leu Arg His Leu Gln Gly His Leu Asn Thr 90 95 100 105	400
tgc agc ttc aat gtc att ccc tgc cct aat cgc tgc ccc atg aag ctg Cys Ser Phe Asn Val Ile Pro Cys Pro Asn Arg Cys Pro Met Lys Leu 110 115 120	448
agc cgc cgt gat cta cct gca cac ttg cag cat gac tgc ccc aag cgg Ser Arg Arg Asp Leu Pro Ala His Leu Gln His Asp Cys Pro Lys Arg 125 130 135	496
cgc ctc aag tgc gag ttt tgt ggc tgt gac ttc agt ggg gag gcc tat Arg Leu Lys Cys Glu Phe Cys Gly Cys Asp Phe Ser Gly Glu Ala Tyr 140 145 150	544
gag agc cat gag ggt atg tgc ccc cag gag agt gtc tac tgt gag aat Glu Ser His Glu Gly Met Cys Pro Gln Glu Ser Val Tyr Cys Glu Asn 155 160 165	592
aag tgt ggt gcc cgc atg atg cgg ggg ctg ctg gcc cag cat gcc acc Lys Cys Gly Ala Arg Met Met Arg Gly Leu Leu Ala Gln His Ala Thr 170 175 180 185	640
tct gag tgc ccc aag cgc act cag ccc tgc acc tac tgc act aag gag Ser Glu Cys Pro Lys Arg Thr Gln Pro Cys Thr Tyr Cys Thr Lys Glu 190 195 200	688
ttc gtc ttt gac acc atc cag agc cac cag tac cag tgc cca agg ctg Phe Val Phe Asp Thr Ile Gln Ser His Gln Tyr Gln Cys Pro Arg Leu 205 210 215	736
cct gtt gcc tgc ccc aac caa tgt ggt gtg ggc act gtg gct cgg gag Pro Val Ala Cys Pro Asn Gln Cys Gly Val Gly Thr Val Ala Arg Glu 220 225 230	784
gac ctg cca ggc cat ctg aag gac agc tgt aac acc gcc ctg gtg ctc Asp Leu Pro Gly His Leu Lys Asp Ser Cys Asn Thr Ala Leu Val Leu 235 240 245	832
tgc cca ttc aaa gac tcc ggc tgc aag cac agg tgc cct aag ctg gca Cys Pro Phe Lys Asp Ser Gly Cys Lys His Arg Cys Pro Lys Leu Ala 250 255 260 265	880
atg gca cgg cat gtg gag gag agt gtg aag cca cat ctg gcc atg atg Met Ala Arg His Val Glu Glu Ser Val Lys Pro His Leu Ala Met Met 270 275 280	928
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gag ctg gag gag cta tca gtg ggc agt gat ggc gtg ctc atc tgg aag Glu Leu Glu Glu Leu Ser Val Gly Ser Asp Gly Val Leu Ile Trp Lys 300 305 310	1024
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ctt gag tgc ttc agc cca gcc ttc tac aca cat aag tat ggt tac aag Leu Glu Cys Phe Ser Pro Ala Phe Tyr Thr His Lys Tyr Gly Tyr Lys 330 335 340 345	1120
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cac ctc tca ctg tac att cgt gtg ctg cct ggt gcc ttt gac aat ctc His Leu Ser Leu Tyr Ile Arg Val Leu Pro Gly Ala Phe Asp Asn Leu 365 370 375	1216
ctt gag tgg ccc ttt gcc cgc cgt gtc acc ttc tcc ctg ctg gat cag Leu Glu Trp Pro Phe Ala Arg Arg Val Thr Phe Ser Leu Leu Asp Gln 380 385 390	1264
agc gac cct ggg ctg gct aaa cca cag cac gtc act gag acc ttc cac Ser Asp Pro Gly Leu Ala Lys Pro Gln His Val Thr Glu Thr Phe His 395 400 405	1312
ccc gac cca aac tgg aag aat ttc cag aag cca ggc acg tgg cgg ggc Pro Asp Pro Asn Trp Lys Asn Phe Gln Lys Pro Gly Thr Trp Arg Gly 410 415 420 425	1360
tcc ctg gat gag agt tct ctg ggc ttt ggt tat ccc aag ttc atc tcc Ser Leu Asp Glu Ser Ser Leu Gly Phe Gly Tyr Pro Lys Phe Ile Ser 430 435 440	1408
cac cag gac att cga aag cga aac tat gtg cggt gat gat gca gtc ttc His Gln Asp Ile Arg Lys Arg Asn Tyr Val Arg Asp Asp Ala Val Phe 445 450 455	1456
atc cgt gct gtt gaa ctg ccc cggt aag atc ctc agc tga Ile Arg Ala Ala Val Glu Leu Pro Arg Lys Ile Leu Ser 460 465 470	1498
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tcccttcttgg gtagggcag acatgccttgg tgccggta cactctacac ggactgaggt gcctgctcag gtgctatgtc ccaagagcca taaggggtg ggaattgggg agggagaaaag	1798 1858
ggtagttcaa agagtctgtc ttgagatctg atttttccctt cctttaccta gctgtcccc ctctgttat ttatccctt agtgccagga gggcacagca ggggagccct gattttaat	1918 1978
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 <213> Homo sapiens
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00-617-F.ST25.txt

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 20 25 30

Thr Cys Gly His Arg Phe Cys Asp Thr Cys Leu Gln Glu Phe Leu Ser
 35 40 45

Glu Gly Val Phe Lys Cys Pro Glu Asp Gln Leu Pro Leu Asp Tyr Ala
 50 55 60

Lys Ile Tyr Pro Asp Pro Glu Leu Glu Val Gln Val Leu Gly Leu Pro
 65 70 75 80

Ile Arg Cys Ile His Ser Glu Glu Gly Cys Arg Trp Ser Gly Pro Leu
 85 90 95

Arg His Leu Gln Gly His Leu Asn Thr Cys Ser Phe Asn Val Ile Pro
 100 105 110

Cys Pro Asn Arg Cys Pro Met Lys Leu Ser Arg Arg Asp Leu Pro Ala
 115 120 125

His Leu Gln His Asp Cys Pro Lys Arg Arg Leu Lys Cys Glu Phe Cys
 130 135 140

Gly Cys Asp Phe Ser Gly Glu Ala Tyr Glu Ser His Glu Gly Met Cys
 145 150 155 160

Pro Gln Glu Ser Val Tyr Cys Glu Asn Lys Cys Gly Ala Arg Met Met
 165 170 175

Arg Gly Leu Leu Ala Gln His Ala Thr Ser Glu Cys Pro Lys Arg Thr
 180 185 190

Gln Pro Cys Thr Tyr Cys Thr Lys Glu Phe Val Phe Asp Thr Ile Gln
 195 200 205

Ser His Gln Tyr Gln Cys Pro Arg Leu Pro Val Ala Cys Pro Asn Gln
 210 215 220

Cys Gly Val Gly Thr Val Ala Arg Glu Asp Leu Pro Gly His Leu Lys
 225 230 235 240

Asp Ser Cys Asn Thr Ala Leu Val Leu Cys Pro Phe Lys Asp Ser Gly
 245 250 255

00-617-F.ST25.txt

Cys Lys His Arg Cys Pro Lys Leu Ala Met Ala Arg His Val Glu Glu
260 265 270

Ser Val Lys Pro His Leu Ala Met Met Cys Ala Leu Val Ser Arg Gln
275 280 285

Arg Gln Glu Leu Gln Glu Leu Arg Arg Glu Leu Glu Glu Leu Ser Val
290 295 300

Gly Ser Asp Gly Val Leu Ile Trp Lys Ile Gly Ser Tyr Gly Arg Arg
305 310 315 320

Leu Gln Glu Ala Lys Ala Lys Pro Asn Leu Glu Cys Phe Ser Pro Ala
325 330 335

Phe Tyr Thr His Lys Tyr Gly Tyr Lys Leu Gln Val Ser Ala Phe Leu
340 345 350

Asn Gly Asn Gly Ser Gly Glu Gly Thr His Leu Ser Leu Tyr Ile Arg
355 360 365

Val Leu Pro Gly Ala Phe Asp Asn Leu Leu Glu Trp Pro Phe Ala Arg
370 375 380

Arg Val Thr Phe Ser Leu Leu Asp Gln Ser Asp Pro Gly Leu Ala Lys
385 390 395 400

Pro Gln His Val Thr Glu Thr Phe His Pro Asp Pro Asn Trp Lys Asn
405 410 415

Phe Gln Lys Pro Gly Thr Trp Arg Gly Ser Leu Asp Glu Ser Ser Leu
420 425 430

Gly Phe Gly Tyr Pro Lys Phe Ile Ser His Gln Asp Ile Arg Lys Arg
435 440 445

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<211> 1105

<212> DNA
<213> Caenorhabditis elegans

00-617-F.ST25.txt

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<400> 14

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Asn	Asn	Ser	Asp	Asp	Thr	Ser	Phe	Ala	Ala	Asp	Arg	Ser	Asn	Ser	Leu	
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ctg	aat	gcg	acg	tgc	ccg	gcg	aga	att	caa	aat	tca	gta	gat	caa	cgg	147
Leu	Asn	Ala	Thr	Cys	Pro	Ala	Arg	Ile	Gln	Asn	Ser	Val	Asp	Gln	Arg	
			35					40					45			

aaa	atc	aat	cga	tca	ttc	aat	gat	tcg	ctg	tcg	tcc	gga	tat	agt	gga	195
Lys	Ile	Asn	Arg	Ser	Phe	Asn	Asp	Ser	Leu	Ser	Ser	Gly	Tyr	Ser	Gly	
			50			55						60				

aaa	tgg	ctt	cgt	cca	aag	cgt	gaa	gcg	ctc	aag	atc	act	cca	ttg	gct	243
Lys	Trp	Leu	Arg	Pro	Lys	Arg	Glu	Ala	Leu	Lys	Ile	Thr	Pro	Leu	Ala	
			65			70					75					

cag	att	gac	gag	gcg	ccg	gca	act	aaa	aga	cat	agc	tcg	gcg	aag	gat	291
Gln	Ile	Asp	Glu	Ala	Pro	Ala	Thr	Lys	Arg	His	Ser	Ser	Ala	Lys	Asp	
			80			85				90						

aag	cac	aca	gaa	tac	aaa	acg	cga	ctt	tgt	gat	gcg	ttc	cgc	cgt	gaa	339
Lys	His	Thr	Glu	Tyr	Lys	Thr	Arg	Leu	Cys	Asp	Ala	Phe	Arg	Arg	Glu	
			95			100			105				110			

gga	tac	tgc	ccg	tac	aac	gac	aat	tgc	aca	tat	gct	cac	gga	caa	gat	387
Gly	Tyr	Cys	Pro	Tyr	Asn	Asp	Asn	Cys	Thr	Tyr	Ala	His	Gly	Gln	Asp	
			115					120				125				

gag	ctg	aga	gtt	ccg	aga	cgc	cgc	caa	gag	tat	tat	tcc	cga	gat	cca	435
Glu	Leu	Arg	Val	Pro	Arg	Arg	Arg	Gln	Glu	Tyr	Tyr	Ser	Arg	Asp	Pro	
			130			135						140				

cca	cgt	gag	cgc	cgt	gat	tct	cgt	tct	aga	cga	gac	gac	gtg	gat	aca	483
Pro	Arg	Glu	Arg	Arg	Asp	Ser	Arg	Ser	Arg	Arg	Asp	Asp	Asp	Val	Asp	
			145			150				155						

aca	atc	aat	cga	tcg	agt	tct	tca	gca	tcg	aag	cat	cat	cat	gat	gag	aat	531
Thr	Ile	Asn	Arg	Ser	Ser	Ser	Ser	Ala	Ser	Lys	His	His	Asp	Glu	Asn		
			160			165				170							

cgg	aga	ccc	agc	aac	aac	cac	gga	agc	tcg	aat	cgt	cgt	cag	att	tgt	579
Arg	Arg	Pro	Ser	Asn	Asn	His	Gly	Ser	Ser	Asn	Arg	Arg	Gln	Ile	Cys	
			175			180			185				190			

cac	aat	ttc	gag	aga	gga	aac	tgc	aga	tat	ggt	cca	aga	tgc	cgc	ttc	627
His	Asn	Phe	Glu	Arg	Gly	Asn	Cys	Arg	Tyr	Gly	Pro	Arg	Cys	Arg	Phe	
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att	cac	gtc	gaa	caa	atg	caa	cat	ttc	aat	gcg	aat	gcg	acg	gtt	tac	675
Ile	His	Val	Glu	Gln	Met	Gln	His	Phe	Asn	Ala	Asn	Ala	Thr	Val	Tyr	
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gcg	cca	cct	tct	tcc	gat	tgt	ccg	ccg	ccg	att	gcc	tac	tac	cat	cat	723
Ala	Pro	Pro	Ser	Ser	Asp	Cys	Pro	Pro	Pro	Ile	Ala	Tyr	Tyr	His	His	

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225	230	235	
cat cca caa cat cag caa caa ttc ctg cca ttt cca atg cca tat ttc His Pro Gln His Gln Gln Phe Leu Pro Phe Pro Met Pro Tyr Phe			771
240	245	250	
ttg gct cca ccg ccg caa gct caa caa gga gct cct ttt cca gtg caa Leu Ala Pro Pro Pro Gln Ala Gln Gln Gly Ala Pro Phe Pro Val Gln			819
255	260	265	270
tat att cca cag caa cat gat ttg atg aat agc cag cca atg tat gca Tyr Ile Pro Gln Gln His Asp Leu Met Asn Ser Gln Pro Met Tyr Ala			867
275	280	285	
cca atg gca ccg aca tac tac tat caa cca att aat tcg aat ggc atg Pro Met Ala Pro Thr Tyr Tyr Tyr Gln Pro Ile Asn Ser Asn Gly Met			915
290	295	300	
ccc atg atg gat gtg act att gat ccg aat gcc acg ggc ggt gcg ttt Pro Met Met Asp Val Thr Ile Asp Pro Asn Ala Thr Gly Gly Ala Phe			963
305	310	315	
gaa gtg ttc ccc gat gga ttc ttc tct cag cca cca act att att Glu Val Phe Pro Asp Gly Phe Phe Ser Gln Pro Pro Pro Thr Ile Ile			1011
320	325	330	
tcc taa ttttgcgtta ttttccatat tttgttttgt atatttatcc actcaccccc Ser			1067
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Ser Asp Asp Thr Ser Phe Ala Ala Asp Arg Ser Asn Ser Leu Leu Asn 20 25 30			
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Asn Arg Ser Phe Asn Asp Ser Leu Ser Ser Gly Tyr Ser Gly Lys Trp 50 55 60			
Leu Arg Pro Lys Arg Glu Ala Leu Lys Ile Thr Pro Leu Ala Gln Ile 65 70 75 80			
Asp Glu Ala Pro Ala Thr Lys Arg His Ser Ser Ala Lys Asp Lys His 85 90 95			

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Thr Glu Tyr Lys Thr Arg Leu Cys Asp Ala Phe Arg Arg Glu Gly Tyr
100 105 110

Cys Pro Tyr Asn Asp Asn Cys Thr Tyr Ala His Gly Gln Asp Glu Leu
115 120 125

Arg Val Pro Arg Arg Arg Gln Glu Tyr Tyr Ser Arg Asp Pro Pro Arg
130 135 140

Glu Arg Arg Asp Ser Arg Ser Arg Arg Asp Asp Val Asp Thr Thr Ile
145 150 155 160

Asn Arg Ser Ser Ser Ser Ala Ser Lys His His Asp Glu Asn Arg Arg
165 170 175

Pro Ser Asn Asn His Gly Ser Ser Asn Arg Arg Gln Ile Cys His Asn
180 185 190

Phe Glu Arg Gly Asn Cys Arg Tyr Gly Pro Arg Cys Arg Phe Ile His
195 200 205

Val Glu Gln Met Gln His Phe Asn Ala Asn Ala Thr Val Tyr Ala Pro
210 215 220

Pro Ser Ser Asp Cys Pro Pro Pro Ile Ala Tyr Tyr His His His Pro
225 230 235 240

Gln His Gln Gln Gln Phe Leu Pro Phe Pro Met Pro Tyr Phe Leu Ala
245 250 255

Pro Pro Pro Gln Ala Gln Gln Gly Ala Pro Phe Pro Val Gln Tyr Ile
260 265 270

Pro Gln Gln His Asp Leu Met Asn Ser Gln Pro Met Tyr Ala Pro Met
275 280 285

Ala Pro Thr Tyr Tyr Tyr Gln Pro Ile Asn Ser Asn Gly Met Pro Met
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Phe Pro Asp Gly Phe Phe Ser Gln Pro Pro Pro Thr Ile Ile Ser
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<211> 2077

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<212> DNA
<213> *Drosophila melanogaster*

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<222> (301)..(1614)

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tcaagtgcaa agcaaataca aatcaaacac aaagaaaaaag caacgaaata aagatata	180	
gaaaagaaaa acaaaaacgaa aaaattcgca catttttct gtcttgtcca gtggaaaata	240	
caacaataa aacaacaacgg ctaaatcaag ttaacaatct gttcaaaacc aatcaacaaa	300	
atg tct gct gat att ctg cag aaa tca aga gag cag gat gat tcg cac	348	
Met Ser Ala Asp Ile Leu Gln Lys Ser Arg Glu Gln Asp Asp Ser His		
1 5 10 15		
tac ttc gag cgt ggc gat ata tcc aaa tac gta acg atg aac gat cac	396	
Tyr Phe Glu Arg Gly Asp Ile Ser Lys Tyr Val Thr Met Asn Asp His		
20 25 30		
ttg ggt gat ttc gat tgc aac gag gtg cgc aag gaa ata agg atg ctg	444	
Leu Gly Asp Phe Asp Cys Asn Glu Val Arg Lys Glu Ile Arg Met Leu		
35 40 45		
ctc gcc cac ggc gcc aac ttg gat cag cag cac cag cag cag cca cat	492	
Leu Ala His Gly Ala Asn Leu Asp Gln Gln His Gln Gln Gln Pro His		
50 55 60		
cgc cac cat ggc ggt ctc aca cgc acc att tca cag ccg gcc cag ctc	540	
Arg His His Gly Gly Leu Thr Arg Thr Ile Ser Gln Pro Ala Gln Leu		
65 70 75 80		
atc cag cag cag cag cag caa cac caa cag cag cag cag cag cag cag	588	
Ile Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln Gln		
85 90 95		
cca cct gtt gcc agt ctg gtg acc atc acc gag aac ctg ggc aac atg	636	
Pro Pro Val Ala Ser Leu Val Thr Ile Thr Glu Asn Leu Gly Asn Met		
100 105 110		
aac ctg cac cga aag ctg gag cga acc caa tcg gag cca ctg ccg cca	684	
Asn Leu His Arg Lys Leu Glu Arg Thr Gln Ser Glu Pro Leu Pro Pro		
115 120 125		
cag cag ccg atg aac aca tcc aga tac aag acc gag ctg tgc cgt ccg	732	
Gln Gln Pro Met Asn Thr Ser Arg Tyr Lys Thr Glu Leu Cys Arg Pro		
130 135 140		
ttc gag gag gcc gga gaa tgc aag tac ggc gag aag tgc cag ttc gcc	780	
Phe Glu Glu Ala Gly Glu Cys Lys Tyr Gly Glu Lys Cys Gln Phe Ala		
145 150 155 160		
cat gga agc cat gag ttg cga aac gtg cac cgt cat ccc aag tac aag	828	
His Gly Ser His Glu Leu Arg Asn Val His Arg His Pro Lys Tyr Lys		
165 170 175		

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acg gaa tac tgc cgc acc ttc cac agc gtg ggc ttc tgt ccc tac gga Thr Glu Tyr Cys Arg Thr Phe His Ser Val Gly Phe Cys Pro Tyr Gly 180 185 190	876
ccg cgc tgt cac ttt gtt cac aat gcg gac gag gcc cgc gcc caa cag Pro Arg Cys His Phe Val His Asn Ala Asp Glu Ala Arg Ala Gln Gln 195 200 205	924
gcf gcc cag gca gcc aag tcc tcc acc cag tcg cag tcg cag tcg cag Ala Ala Gln Ala Ala Lys Ser Ser Thr Gln Ser Gln Ser Gln Ser Gln 210 215 220	972
cag tcg tcg tcg cag aac ttc tcg ccg aag agc aac cag agc agc aat Gln Ser Ser Ser Gln Asn Phe Ser Pro Lys Ser Asn Gln Ser Ser Asn 225 230 235 240	1020
caa agt agc aac agt agc agc agc agc agc agc ggc ggc ggc ggt Gln Ser Ser Asn Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly Gly 245 250 255	1068
ggc ggc ggc aac agc atc aac aac aac ggt agc caa ttc tat ctg Gly Gly Gly Asn Ser Ile Asn Asn Asn Gly Ser Gln Phe Tyr Leu 260 265 270	1116
ccg cta agc cca ccg ctg agc atg agc aca gga tcg gac cgg gaa tcg Pro Leu Ser Pro Pro Leu Ser Met Ser Thr Gly Ser Asp Arg Glu Ser 275 280 285	1164
ccc acc gga tca ctg tcc ctc agc ccc acc aac tcg ttg acc agc ttc Pro Thr Gly Ser Leu Ser Leu Ser Pro Thr Asn Ser Leu Thr Ser Phe 290 295 300	1212
ccg ttc cac gat gcc ctg cag cat gga tat ttg gca tcg aat ggc gcc Pro Phe His Asp Ala Leu Gln His Gly Tyr Leu Ala Ser Asn Gly Ala 305 310 315 320	1260
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ctg ggc atg agc atg ggc atc ggc cag ggc atg atc atc ggt cag ggt Leu Gly Met Ser Met Gly Ile Gly Gln Gly Met Ile Ile Gly Gln Gly 340 345 350	1356
ttg gga atg gga cat cat gga ccg gcc aca ccg ccg gag agc ccc aat Leu Gly Met Gly His His Gly Pro Ala Thr Pro Pro Glu Ser Pro Asn 355 360 365	1404
gtg ccc ata tcg cca gtg cat aca cca cca ccg tac gat gtg gtg gtc Val Pro Ile Ser Pro Val His Thr Pro Pro Pro Tyr Asp Val Val Val 370 375 380	1452
agt gga tct gga gcg ggc aac aat agc gtt ggc agc aag cag ctc ctg Ser Gly Ser Gly Ala Gly Asn Asn Ser Val Gly Ser Lys Gln Leu Leu 385 390 395 400	1500
cag aag agc gtc agc aca ccg atg cag cag gag gat acg ccc agg ttg Gln Lys Ser Val Ser Thr Pro Met Gln Gln Glu Asp Thr Pro Arg Leu 405 410 415	1548
ccg gtt ttc aac cgt ctc agc tcc ggt gtg gag gcc tac cag cag cag Pro Val Phe Asn Arg Leu Ser Ser Gly Val Glu Ala Tyr Gln Gln Gln 420 425 430	1596

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Ser Asn Leu Gly Leu	
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gcatccttga caaaatctca gtaacgacca aaccatggaa actgaaaaca aaactactct	1764
cgcagtccaa tttgaaacgc aaatatgccca aggcaaattgg atttccggtg gcgttaacttc	1824
gttgtcagaat aagtgtgtat caagtatacg ccaaacacag acacccctta attatgaacc	1884
gatccttgat atcaattctc tcattgctgt gacagtcaaa cgtaatcggtt atacaataat	1944
cgttatatga gaaggaccga attacggact actacgggac aatttagttag atagatacgt	2004
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<211> 437
<212> PRT
<213> Drosophila melanogaster

<400> 17

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Leu Gly Asp Phe Asp Cys Asn Glu Val Arg Lys Glu Ile Arg Met Leu
35 40 45

Leu Ala His Gly Ala Asn Leu Asp Gln Gln His Gln Gln Gln Pro His
50 55 60

Arg His His Gly Gly Leu Thr Arg Thr Ile Ser Gln Pro Ala Gln Leu
65 70 75 80

Ile Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln
85 90 95

Pro Pro Val Ala Ser Leu Val Thr Ile Thr Glu Asn Leu Gly Asn Met
100 105 110

Asn Leu His Arg Lys Leu Glu Arg Thr Gln Ser Glu Pro Leu Pro Pro
115 120 125

Gln Gln Pro Met Asn Thr Ser Arg Tyr Lys Thr Glu Leu Cys Arg Pro
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Phe Glu Glu Ala Gly Glu Cys Lys Tyr Gly Glu Lys Cys Gln Phe Ala
145 150 155 160

His Gly Ser His Glu Leu Arg Asn Val His Arg His Pro Lys Tyr Lys
165 170 175

Thr Glu Tyr Cys Arg Thr Phe His Ser Val Gly Phe Cys Pro Tyr Gly
180 185 190

Pro Arg Cys His Phe Val His Asn Ala Asp Glu Ala Arg Ala Gln Gln
195 200 205

Ala Ala Gln Ala Ala Lys Ser Ser Thr Gln Ser Gln Ser Gln
210 215 220

Gln Ser Ser Ser Gln Asn Phe Ser Pro Lys Ser Asn Gln Ser Ser Asn
225 230 235 240

Gln Ser Ser Asn Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly
245 250 255

Gly Gly Gly Asn Ser Ile Asn Asn Asn Asn Gly Ser Gln Phe Tyr Leu
260 265 270

Pro Leu Ser Pro Pro Leu Ser Met Ser Thr Gly Ser Asp Arg Glu Ser
275 280 285

Pro Thr Gly Ser Leu Ser Leu Ser Pro Thr Asn Ser Leu Thr Ser Phe
290 295 300

Pro Phe His Asp Ala Leu Gln His Gly Tyr Leu Ala Ser Asn Gly Ala
305 310 315 320

Lys Ser Asn Ser Ser Ala Ser Ser Thr Ser Ser Ala Ser Gly Met Gly
325 330 335

Leu Gly Met Ser Met Gly Ile Gly Gln Gly Met Ile Ile Gly Gln Gly
340 345 350

Leu Gly Met Gly His His Gly Pro Ala Thr Pro Pro Glu Ser Pro Asn
355 360 365

Val Pro Ile Ser Pro Val His Thr Pro Pro Pro Tyr Asp Val Val Val
370 375 380

Ser Gly Ser Gly Ala Gly Asn Asn Ser Val Gly Ser Lys Gln Leu Leu
Page 43

Gln Lys Ser Val Ser Thr Pro Met Gln Gln Glu Asp Thr Pro Arg Leu
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Pro Val Phe Asn Arg Leu Ser Ser Gly Val Glu Ala Tyr Gln Gln Gln
420 425 430

Ser Asn Leu Gly Leu
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<213> *Homo sapiens*

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<222> (774)..(1733)

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gaaccttaggg caaagagttt tattttcagg aatcacatcc ctgtctcccc caacctcaga 180
ccaggcccccc aatctcctcc ccacaagaaa aagcaaaggc agtctgaaaa cctgttgcca 240
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Gly
1

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Asn Lys Met Leu Asn Tyr Ser Ala Pro Ser Ala Gly Gly Cys Leu Leu
5 10 15

gac aga aag gca gtg ggc acc cct gct ggt ggg ggc ttc cct cg²⁰g agg
 Asp Arg Lys Ala Val Gly Thr Pro Ala Gly Gly Gly Phe Pro Arg Arg
872

cac tca gtc acc ctc ccc agc tcc aag ttc cac cag aac cag ctc ctc 920

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His	Ser	Val	Thr	Leu	Pro	Ser	Ser	Lys	Phe	His	Gln	Asn	Gln	Leu	Leu	
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Ser	Ser	Leu	Lys	Gly	Glu	Pro	Ala	Pro	Ala	Leu	Ser	Ser	Arg	Asp	Ser	
50				55				60								65
cgc	ttc	cga	gac	cgc	tcc	ttc	tcg	gaa	ggg	ggc	gag	cgg	ctg	ctg	ccc	1016
Arg	Phe	Arg	Asp	Arg	Ser	Phe	Ser	Glu	Gly	Gly	Glu	Arg	Leu	Leu	Pro	
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acc	cag	aag	cag	ccc	ggg	ggc	ggc	cag	gtc	aac	tcc	agc	cgc	tac	aag	1064
Thr	Gln	Lys	Gln	Pro	Gly	Gly	Gly	Gln	Val	Asn	Ser	Ser	Arg	Tyr	Lys	
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Thr	Glu	Leu	Cys	Arg	Pro	Phe	Glu	Glu	Asn	Gly	Ala	Cys	Lys	Tyr	Gly	
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gac	aag	tgc	cag	ttc	gca	cac	ggc	atc	cac	gag	ctc	cgc	agc	ctg	acc	1160
Asp	Lys	Cys	Gln	Phe	Ala	His	Gly	Ile	His	Glu	Leu	Arg	Ser	Leu	Thr	
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cgc	cac	ccc	aag	tac	aag	acg	gag	ctg	tgc	cgc	acc	ttc	cac	acc	atc	1208
Arg	His	Pro	Lys	Tyr	Lys	Thr	Glu	Leu	Cys	Arg	Thr	Phe	His	Thr	Ile	
							135									130
ggc	ttt	tgc	ccc	tac	ggg	ccc	cgc	tgc	cac	ttc	atc	cac	aac	gct	gaa	1256
Gly	Phe	Cys	Pro	Tyr	Gly	Pro	Arg	Cys	His	Phe	Ile	His	Asn	Ala	Glu	
							150									155
gag	cgc	cgt	gcc	ctg	gcc	ggg	gcc	cgg	gac	ctc	tcc	gct	gac	cgt	ccc	1304
Glu	Arg	Arg	Ala	Leu	Ala	Gly	Ala	Arg	Asp	Leu	Ser	Ala	Asp	Arg	Pro	
							165									170
cgc	ctc	cag	cat	agc	ttt	agc	ttt	gct	ggg	ttt	ccc	agt	gcc	gct	gcc	1352
Arg	Leu	Gln	His	Ser	Phe	Ser	Phe	Ala	Gly	Phe	Pro	Ser	Ala	Ala	Ala	
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Thr	Ala	Ala	Ala	Thr	Gly	Leu	Leu	Asp	Ser	Pro	Thr	Ser	Ile	Thr	Pro	
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ccc	cct	att	ctg	agc	gcc	gat	gac	ctc	ctg	ggc	tca	cct	acc	ctg	ccc	1448
Pro	Pro	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Leu	Gly	Ser	Pro	Thr	Leu	Pro	
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gat	ggc	acc	aat	aac	cct	ttt	gcc	ttc	tcc	agc	cag	gag	ctg	gca	agc	1496
Asp	Gly	Thr	Asn	Asn	Pro	Phe	Ala	Phe	Ser	Ser	Gln	Glu	Leu	Ala	Ser	
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ctc	ttt	gcc	cct	agc	atg	ggg	ctg	ccc	ggg	ggt	ggc	tcc	ccg	acc	acc	1544
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Phe	Leu	Phe	Arg	Pro	Met	Ser	Glu	Ser	Pro	His	Met	Phe	Asp	Ser	Pro	
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ccc	agc	cct	cag	gat	tct	ctc	tcg	gac	cag	gag	ggc	tac	ctg	agc	agc	1640
Pro	Ser	Pro	Gln	Asp	Ser	Leu	Ser	Asp	Gln	Glu	Gly	Tyr	Leu	Ser	Ser	
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																285

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aga cgc ctg ccc atc ttc agc aga ctt tcc atc tca gat gac taa Arg Arg Leu Pro Ile Phe Ser Arg Leu Ser Ile Ser Asp Asp 310 315	1733
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ggcagtttgc tgcacttaga gggcacgggg tggaggtttt ctgcaaagga gcctgtactt	3833
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 <213> Homo sapiens

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Arg His Ser Val Thr Leu Pro Ser Ser Lys Phe His Gln Asn Gln Leu
 35 40 45

Leu Ser Ser Leu Lys Gly Glu Pro Ala Pro Ala Leu Ser Ser Arg Asp
 50 55 60

Ser Arg Phe Arg Asp Arg Ser Phe Ser Glu Gly Gly Glu Arg Leu Leu
 65 70 75 80

Pro Thr Gln Lys Gln Pro Gly Gly Gln Val Asn Ser Ser Arg Tyr
 85 90 95

Lys Thr Glu Leu Cys Arg Pro Phe Glu Glu Asn Gly Ala Cys Lys Tyr
 100 105 110

Gly Asp Lys Cys Gln Phe Ala His Gly Ile His Glu Leu Arg Ser Leu
 115 120 125

Thr Arg His Pro Lys Tyr Lys Thr Glu Leu Cys Arg Thr Phe His Thr
 130 135 140

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Ile Gly Phe Cys Pro Tyr Gly Pro Arg Cys His Phe Ile His Asn Ala
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Glu Glu Arg Arg Ala Leu Ala Gly Ala Arg Asp Leu Ser Ala Asp Arg
165 170 175

Pro Arg Leu Gln His Ser Phe Ser Phe Ala Gly Phe Pro Ser Ala Ala
180 185 190

Ala Thr Ala Ala Ala Thr Gly Leu Leu Asp Ser Pro Thr Ser Ile Thr
195 200 205

Pro Pro Pro Ile Leu Ser Ala Asp Asp Leu Leu Gly Ser Pro Thr Leu
210 215 220

Pro Asp Gly Thr Asn Asn Pro Phe Ala Phe Ser Ser Gln Glu Leu Alan
225 230 235 240

Ser Leu Phe Ala Pro Ser Met Gly Leu Pro Gly Gly Gly Ser Pro Thr
245 250 255

Thr Phe Leu Phe Arg Pro Met Ser Glu Ser Pro His Met Phe Asp Ser
260 265 270

Pro Pro Ser Pro Gln Asp Ser Leu Ser Asp Gln Glu Gly Tyr Leu Ser
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Pro	Asn	Ala	Asn	Ser	Thr	Ser	Thr	Thr	Ser	Ser	Ile	Phe	Ser	Asp		
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Leu	Asn	Lys	Glu	Tyr	Glu	Ser	Lys	Ile	Lys	Glu	Ile	Glu	Glu	Tyr	Tyr	
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ata	aag	aca	ctg	ctc	aat	gaa	aat	acc	gat	aat	gat	gac	agc	agc	agc	612
Ile	Lys	Thr	Leu	Leu	Asn	Glu	Asn	Thr	Asp	Asn	Asp	Asp	Ser	Ser	Ser	
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Ser	Glu	Gly	His	Asn	Ile	Asn	Glu	Thr	Asp	Ile	Leu	Ser	Glu	Tyr	Ser	
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Thr	Leu	Pro	Ile	Asn	Asn	Pro	Phe	Ala	Gly	Asn	Asn	Asn	Ile	Ser	Thr	
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Val	Asn	Pro	Thr	Tyr	Thr	Ser	Ala	Phe	Ser	Leu	Pro	Leu	Thr	Ala		
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gag	aat	tta	caa	aaa	cta	tct	cag	gtg	gat	tct	cag	tct	act	gga	ctt	948
Glu	Asn	Leu	Gln	Lys	Leu	Ser	Gln	Val	Asp	Ser	Gln	Ser	Thr	Gly	Leu	
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cca	tac	aca	ctt	cca	att	cag	aaa	aca	aca	aaa	ctg	gaa	cct	tgt	aga	996
Pro	Tyr	Thr	Leu	Pro	Ile	Gln	Lys	Thr	Thr	Lys	Leu	Glu	Pro	Cys	Arg	
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Arg	Ala	Pro	Leu	Gln	Leu	Pro	Gln	Leu	Val	Asn	Lys	Thr	Leu	Tyr	Lys	
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Thr	Glu	Leu	Cys	Glu	Ser	Phe	Thr	Ile	Lys	Gly	Tyr	Cys	Lys	Tyr	Gly	
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Lys Ser Asn Asn Tyr Arg Thr Lys Pro Cys Ile Asn Trp Ser Lys Leu	
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ggc tac tgt ccg tac ggt aag cgt tgc tgt ttc aaa cac ggt gat gat	1236
Gly Tyr Cys Pro Tyr Gly Lys Arg Cys Cys Phe Lys His Gly Asp Asp	
255 260 265 270	
aag gac gtt gaa ata tat caa aat gct aac gat gga aga agt aag gat	1284
Lys Asp Val Glu Ile Tyr Gln Asn Ala Asn Asp Gly Arg Ser Lys Asp	
275 280 285	
acg gcg ttg act cca ctt cct act tcc cta gcc cca agc aac aac gat	1332
Thr Ala Leu Thr Pro Leu Pro Thr Ser Leu Ala Pro Ser Asn Asn Asp	
290 295 300	
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Asn Ile Thr Asn Leu Ser Lys Pro Arg Asn Leu His Thr Ser Val Lys	
305 310 315	
gca ttg caa agg atg act tgg tag tcggtaaca acaaaggccct ttgaatattt	1434
Ala Leu Gln Arg Met Thr Trp	
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Lys Glu Tyr Glu Ser Lys Ile Lys Glu Ile Glu Glu Tyr Tyr Ile Lys	
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Thr Leu Leu Asn Glu Asn Thr Asp Asn Asp Asp Ser Ser Ser Ser Glu	
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Gly His Asn Ile Asn Glu Thr Asp Ile Leu Ser Glu Tyr Ser Pro Arg	
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Pro Ser Pro Trp Leu Pro Ser Lys Pro Asn Cys Tyr His Pro Leu Gly	
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Asp Phe Lys Asp Leu Ile Ile Ser Asp Ser Arg Pro Thr Asn Thr Leu
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Pro Ile Asn Asn Pro Phe Ala Gly Asn Asn Asn Ile Ser Thr Leu Ala
 115 120 125

Thr Thr Glu Lys Lys Arg Lys Lys Arg Ser Leu Glu Val Arg Val Asn
 130 135 140

Pro Thr Tyr Thr Thr Ser Ala Phe Ser Leu Pro Leu Thr Ala Glu Asn
 145 150 155 160

Leu Gln Lys Leu Ser Gln Val Asp Ser Gln Ser Thr Gly Leu Pro Tyr
 165 170 175

Thr Leu Pro Ile Gln Lys Thr Thr Lys Leu Glu Pro Cys Arg Arg Ala
 180 185 190

Pro Leu Gln Leu Pro Gln Leu Val Asn Lys Thr Leu Tyr Lys Thr Glu
 195 200 205

Leu Cys Glu Ser Phe Thr Ile Lys Gly Tyr Cys Lys Tyr Gly Asn Lys
 210 215 220

Cys Gln Phe Ala His Gly Leu Asn Glu Leu Lys Phe Lys Lys Lys Ser
 225 230 235 240

Asn Asn Tyr Arg Thr Lys Pro Cys Ile Asn Trp Ser Lys Leu Gly Tyr
 245 250 255

Cys Pro Tyr Gly Lys Arg Cys Cys Phe Lys His Gly Asp Asp Lys Asp
 260 265 270

Val Glu Ile Tyr Gln Asn Ala Asn Asp Gly Arg Ser Lys Asp Thr Ala
 275 280 285

Leu Thr Pro Leu Pro Thr Ser Leu Ala Pro Ser Asn Asn Asp Asn Ile
 290 295 300

Thr Asn Leu Ser Lys Pro Arg Asn Leu His Thr Ser Val Lys Ala Leu
 305 310 315 320

Gln Arg Met Thr Trp
 325